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Abstracts

Evolution of Development

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New genetic and genomic tools for the study of floral evolution

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The angiosperm genus *Aquilegia* presents a unique opportunity to investigate the molecular genetic changes underlying a recent adaptive radiation that involved floral and ecological diversification. In addition, *Aquilegia* has the benefit of representing a phylogenetic lineage that is intermediate between core eudicot model species like *Arabidopsis* and monocot models, such as rice. This combination of assets (and small ~350 Mb genome size) places *Aquilegia* in the singular position of facilitating studies of both recent and ancient evolutionary processes. By the application of innovative genomic techniques, we are developing a wide array of tools that will enable a whole community of researchers to study adaptation at the genomic level. In addition, we are pursuing candidate gene approaches aimed at understanding several genetic pathways including floral organ identity and flowering time control. To these ends, we have identified homologs of all of the *Arabidopsis* floral organ identity genes in *Aquilegia*, and have begun to characterize their expression patterns in both wildtype and mutant plants. It appears that gene duplications which occurred in the *APETALA3* lineage before the diversification of the Ranunculaceae have facilitated the evolution of multiple forms of petaloid organs in this new model species. This theory is being evaluated through genetic analyses of homeotic mutants that affect the identity of petaloid organs.

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The evolution of plant form: An example from maize

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Maize is a domesticated form of a wild Mexican grass called teosinte. The domestication of maize from teosinte occurred about 8000 years ago. As a result of human (artificial) selection during the domestication process, dramatic changes in morphology arose such that maize no longer closely resembles its teosinte ancestor in ear and plant architecture. Quantitative trait locus (QTL) mapping has shown that many genes contributed to the differences between maize and teosinte, but among these are several of very large effect. We have cloned and analyzed two of these large_effect genes. teosinte branched (tb1) is largely responsible for the difference between the long branches of teosinte versus the short branches of maize. tb1 encodes a transcriptional regulator that functions as a repressor of branch elongation. Gene expression analysis indicates that the product of the teosinte allele of tb1 accumulates at about half the level of the maize allele. Fine_mapping experiments show that the differences in phenotype and gene expression are controlled by an enhancer that is 65 kb upstream of the ORF. teosinte glume architecture (tga1) is largely responsible for the formation of a casing that surrounds teosinte seeds but is lacking in maize. tga1 also encodes a transcriptional regulator, however in this case a single amino acid change appears to represent the functional difference between maize and teosinte. Overall, our work and that of other lab groups are beginning to reveal the nature of the genetic and developmental changes underlying the evolution of new morphologies in plants.

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Patterning domains in the vertebrate mesoderm

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The body plan of vertebrates comprises an axial system of a cranium and segmental vertebrae. In jawed vertebrates the axial system is integrated with an appendicular system, the paired fins or limbs and their girdles. In a developmental sense, this body plan is conserved throughout the lineage. The appendicular skeletal elements arise from the lateral plate mesoderm (LP) and the axial skeleton arises from the paraxial somites. All of the striated muscles for both systems arise from the somitic myotomes. Despite the conservation of this embryological pattern, the final morphological outcome is extremely diverse,

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